

PF 30-APR-2001; 2001WO-DK000293.

XX 28-APR-2000; 2000DK-00000707.

PR 10-MAY-2000; 2000US-0203345P.

PR 28-FEB-2001; 2001DK-00000327.

PR 21-MAR-2001; 2001US-0277817P.

XX (NOVO ) NOVOZYMES AS.

XX Roggen EL, Ernst S, Svendsen A, Friis EP, Von Der Osten C;

XX WPI; 2001-626552/72.

XX Selecting protein variants having modified immunogenicity, used to

XX produce vaccines, detergents and personal care compositions, involves

XX localizing epitope sequences on the three-dimensional structure of a

XX protein.

XX Claim 99; Page 510-512; 513pp; English.

XX The invention relates to selecting a protein variant having modified

XX immunogenicity, compared to a parent protein, comprising using the

XX antibody binding sequence to localise epitope sequences on the three

XX dimensional structure of the parent protein and defining an epitope area

XX including amino acids within 5 Angstrom of the epitope amino acids. The

XX method is useful for identifying structural epitopes on the 3-dimensional

XX surface of commercial and environmental allergens. Compositions

XX containing the protein variants are used as vaccines, detergents and

XX personal care compositions, e.g. shampoo, balsam, hair conditioners, hair

XX waving compositions, hair dyeing compositions, hair tonic, hair liquid,

XX hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen,

XX shaving foam, cream soap, skin milk or foundation. The present sequence

XX is that of a polypeptide of the invention

XX SQ Sequence 471 AA;

Query Match 92.7%; Score 1440; DB 4; Length 471;

Best Local Similarity 100.0%; Pred. No. 1.2e-133;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

25 ATLDLSWLSNEATVARTALNNIGADGAWVSGADSGIIVASPSSTNDPFIYTWTRDGLVL 84

1 ATLDLSWLSNEATVARTALNNIGADGAWVSGADSGIIVASPSSTNDPFIYTWTRDGLVL 60

85 KTLVDLFRNGDTSLLSTIENYISAQAIYVQGISNPSGDLSSGAGLGEKPFNVDEYATGSM 144

61 KTLVDLFRNGDTSLLSTIENYISAQAIYVQGISNPSGDLSSGAGLGEKPFNVDEYATGSM 120

145 GRPQDGPALRATAMIGFGQWLLDNGYTSATDIWPLVRNDLSYVAQYWNQTYDLWEE 204

121 GRPQDGPALRATAMIGFGQWLLDNGYTSATDIWPLVRNDLSYVAQYWNQTYDLWEE 180

205 VNGSSFFTTIAVQHRALVEGSAFATVAGSSCWDCSQAPEILCYLQSFWTGSFILANFDS 264

181 VNGSSFFTTIAVQHRALVEGSAFATVAGSSCWDCSQAPEILCYLQSFWTGSFILANFDS 240

265 RSGKDANTLLGSIHTFDPPEACDDSTFPQCS 295

241 RSGKDANTLLGSIHTFDPPEACDDSTFPQCS 271

RESULT 12

AAW55979

ID AAW55979 standard; protein; 616 AA.

XX AAW55979;

XX 27-JUL-1998 (first entry)

XX Aspergillus awamori glucoamylase mutant S411A.

XX Aspergillus awamori; glucoamylase; Aspergillus sp; mutant; fungal; food;

XX fructose; corn; sweetener; 1,4-alpha-D-glucon glucohydrolase;

XX

KW genetic engineering.

XX Synthetic.

OS Aspergillus awamori.

PN WO9803639-A1.

XX 29-JAN-1998.

XX 24-JUL-1997; 97WO-US012983.

XX 24-JUL-1996; 96US-0022578P.

XX 02-AUG-1996; 96US-0023077P.

XX (IOWA ) UNIV IOWA STATE RES FOUND INC.

XX Allen M, Fang T, Li Y, Liu H, Chen H, Coutinho P, Honzatko R;

XX Ford C;

XX WPI; 1998-120764/11.

XX Genetically engineered fungal glucoamylase - useful in, e.g. food

XX industry for production of high fructose corn sweeteners.

XX Claim 10; Page; 97pp; English.

XX The present sequence represents a specifically claimed mutant

XX glucoamylase from Aspergillus awamori (1,4-alpha-D-glucon

XX glucosylase). The present invention describes fungal glucoamylases

XX (FG) comprising: a mutation pair Asn20Cys coupled with Ala27Cys forming a

XX disulphide bond between the 2 members of the pair; and a 311-314Loop or

XX Ser411Ala mutation. FG can be used in industry for the production of high

XX fructose corn sweeteners, while the glucose produced by glucoamylase can

XX be crystallised or used in fermentation to produce organic products, e.g.

XX citric acid, ascorbic acid, lysine, glutamic acid or ethanol for

XX beverages and fuel. The mutations provide increased thermal stability,

XX reduced isomaltose formation and increased pH optimum. N.B. The present

XX sequence is not given in the specification but is derived from SEQ ID

XX NO:1 as stated in the claim

XX SQ Sequence 616 AA;

Query Match 92.7%; Score 1440; DB 2; Length 616;

Best Local Similarity 100.0%; Pred. No. 1.8e-133;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

25 ATLDLSWLSNEATVARTALNNIGADGAWVSGADSGIIVASPSSTNDPFIYTWTRDGLVL 84

1 ATLDLSWLSNEATVARTALNNIGADGAWVSGADSGIIVASPSSTNDPFIYTWTRDGLVL 60

85 KTLVDLFRNGDTSLLSTIENYISAQAIYVQGISNPSGDLSSGAGLGEKPFNVDEYATGSM 144

61 KTLVDLFRNGDTSLLSTIENYISAQAIYVQGISNPSGDLSSGAGLGEKPFNVDEYATGSM 120

145 GRPQDGPALRATAMIGFGQWLLDNGYTSATDIWPLVRNDLSYVAQYWNQTYDLWEE 204

121 GRPQDGPALRATAMIGFGQWLLDNGYTSATDIWPLVRNDLSYVAQYWNQTYDLWEE 180

205 VNGSSFFTTIAVQHRALVEGSAFATVAGSSCWDCSQAPEILCYLQSFWTGSFILANFDS 264

181 VNGSSFFTTIAVQHRALVEGSAFATVAGSSCWDCSQAPEILCYLQSFWTGSFILANFDS 240

265 RSGKDANTLLGSIHTFDPPEACDDSTFPQCS 295

241 RSGKDANTLLGSIHTFDPPEACDDSTFPQCS 271

RESULT 13

AAI515176

ID AAI515176 standard; protein; 616 AA.

XX AAI515176;

XX